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PATENT APPLICATION: US/10/049,407

DATE: 02/27/2002

TIME: 13:23:41

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3 <110> APPLICANT: Denton, R. Rex
4     Kliem, Stefanie
5     Nandabalan, Krishnan
6     Stephens, J. Claiborne
8 <120> TITLE OF INVENTION: DRUG TARGET ISOGENES: POLYMORPHISMS IN THE
9     5-HYDROXYTRYPTAMINE RECEPTOR 1A GENE
11 <130> FILE REFERENCE: MWH-0006US HTR1A
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/049,407
14 <141> CURRENT FILING DATE: 2002-02-06
16 <150> PRIOR APPLICATION NUMBER: PCT/US00/40519
17 <151> PRIOR FILING DATE: 2000-08-06
19 <150> PRIOR APPLICATION NUMBER: 60/147,711
20 <151> PRIOR FILING DATE: 1999-08-06
22 <160> NUMBER OF SEQ ID NOS: 53
24 <170> SOFTWARE: PatentIn Ver. 2.1
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29 <213> ORGANISM: Homo sapiens
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42 cacagaggga taaataaagg gaagtgagga ggaagaggga gacttaaagg gaaggcagg 660
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56 <211> LENGTH: 1938

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57 <212> TYPE: DNA

58 <213> ORGANISM: Homo sapiens

60 <400> SEQUENCE: 2

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65 gccgaagcag taagaacttc ctgcttgggt ctctgcattc ccttctccg aaacttccca 300
66 ggagaaggcg ggaagacccc aggggaaggg gcgaggcgaa tcttcgcgct gctttttctt 360
67 cctccccct tcccgcgcg ggcgcgcgagg catggatgtg ctccagccctg gtcagggcaa 420
68 caacaccaca tcaccaccgg ctccctttga gaccggcggc aacactactg gtatctccga 480
69 cgtgaccgtc agctaccaag tgatcacctc tctgctgctg ggcacgctca tcttctgcgc 540
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91 gtcccctccc cacttctgct tccacggcag ggccctttgt gcaaaggaga cccagcgagg 1860
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99 <213> ORGANISM: Homo sapiens

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104 agtgcaatgg cgcgagaacg gaggtagctt tttaaaaacg aagacacact cggctcttct 180
105 ccatcaatta gcaataattg ggagactgac ccaggactgt tcacctccc attcaggctc 240
106 cctatgcttc cttttctcat ctctattgc cactctgga tgctgacacg atttaagaat 300
107 ttggcagata atatgaccca aggagtgtt ggaattccct ccccaagtt tttccaaccc 360
108 cagttttgtt ggggtggagg cggagtatt ttgttacaac cttggtctga ccggcaggga 420
109 cctgggtgtg gtaagttagt tctgagtctc tgttgacaaa aagagactcg aatgcaaaga 480

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112 cacagaggga taaataaagg gaagttagga ggaagaggga gacttaaagg gaaggcaggt 660
113 ggggagaagg gggacgaaag aggcagaaga gagagaagag aggaggagag agggggagag 720
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123 ccgacgtgac cgtcagctac caagtgatca cctctctgct gctgggcaag ctcatcttct 1320
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160 accgacctca tgggtgctgg gttggtgctg cccatggccg cgctgtatca ggtgctcaac 300
161 aagtggacac tgggcccagg aacctgcgac ctgttcatcg ccctcgacgt gctgtgctgc 360

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173 aggaagacag tgaagacgct gggcatcatc atgggcacct tcatcctctg ctggctgccc 1080
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175 ttgggcgcca taatcaattg gctgggctac tccaactctc tgcttaacct cgtcatttac 1200
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190 20 25 30
192 Val Ser Tyr Gln Val Ile Thr Ser Leu Leu Leu Gly Thr Leu Ile Phe
193 35 40 45
195 Cys Ala Val Leu Gly Asn Ala Cys Val Val Ala Ala Ile Ala Leu Glu
196 50 55 60
198 Arg Ser Leu Gln Asn Val Ala Asn Tyr Leu Ile Gly Ser Leu Ala Val
199 65 70 75 80
201 Thr Asp Leu Met Val Ser Val Leu Val Leu Pro Met Ala Ala Leu Tyr
202 85 90 95
204 Gln Val Leu Asn Lys Trp Thr Leu Gly Gln Val Thr Cys Asp Leu Phe
205 100 105 110
207 Ile Ala Leu Asp Val Leu Cys Cys Thr Ser Ser Ile Leu His Leu Cys
208 115 120 125
210 Ala Ile Ala Leu Asp Arg Tyr Trp Ala Ile Thr Asp Pro Ile Asp Tyr
211 130 135 140
213 Val Asn Lys Arg Thr Pro Arg Arg Ala Ala Ala Leu Ile Ser Leu Thr
214 145 150 155 160
216 Trp Leu Ile Gly Phe Leu Ile Ser Ile Pro Pro Met Leu Gly Trp Arg
217 165 170 175
219 Thr Pro Glu Asp Arg Ser Asp Pro Asp Ala Cys Thr Ile Ser Lys Asp
220 180 185 190
222 His Gly Tyr Thr Ile Tyr Ser Thr Phe Gly Ala Phe Tyr Ile Pro Leu
223 195 200 205
225 Leu Leu Met Leu Val Leu Tyr Gly Arg Ile Phe Arg Ala Ala Arg Phe
226 210 215 220

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228 Arg Ile Arg Lys Thr Val Lys Lys Val Glu Lys Thr Gly Ala Asp Thr
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231 Arg His Gly Ala Ser Pro Ala Pro Gln Pro Lys Lys Ser Val Asn Gly
232                245                250                255
234 Glu Ser Gly Ser Arg Asn Trp Arg Leu Gly Val Glu Ser Lys Ala Gly
235                260                265                270
237 Gly Ala Leu Cys Ala Asn Gly Ala Val Arg Gln Gly Asp Asp Gly Ala
238                275                280                285
240 Ala Leu Glu Val Ile Glu Val His Arg Val Gly Asn Ser Lys Glu His
241                290                295                300
243 Leu Pro Leu Pro Ser Glu Ala Gly Pro Thr Pro Cys Ala Pro Ala Ser
244 305                310                315                320
246 Phe Glu Arg Lys Asn Glu Arg Asn Ala Glu Ala Lys Arg Lys Met Ala
247                325                330                335
249 Leu Ala Arg Glu Arg Lys Thr Val Lys Thr Leu Gly Ile Ile Met Gly
250                340                345                350
252 Thr Phe Ile Leu Cys Trp Leu Pro Phe Phe Ile Val Ala Leu Val Leu
253                355                360                365
255 Pro Phe Cys Glu Ser Ser Cys His Met Pro Thr Leu Leu Gly Ala Ile
256                370                375                380
258 Ile Asn Trp Leu Gly Tyr Ser Asn Ser Leu Leu Asn Pro Val Ile Tyr
259 385                390                395                400
261 Ala Tyr Phe Asn Lys Asp Phe Gln Asn Ala Phe Lys Lys Ile Ile Lys
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265 420

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270 <212> TYPE: DNA

271 <213> ORGANISM: Homo sapiens

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279 <212> TYPE: DNA

280 <213> ORGANISM: Homo sapiens

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298 <213> ORGANISM: Homo sapiens

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